

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/539,725

Source:

PAT

Date Processed by STIC:

6/29/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENT IN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/539,725

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☒ Use of <220> Sequence(s) 120, 86 missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/539,725

DATE: 06/29/2005

TIME: 14:07:59

Input Set : E:\05-06-06 1041WO.txt

Output Set: N:\CRF4\06292005\J539725.raw

3 <110> APPLICANT: greenovation Biotech GmbH
 5 <120> TITLE OF INVENTION: Improvements in or relating to protein production
 7 <130> FILE REFERENCE: Protein Production Method
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/539,725
 C--> 11 <141> CURRENT FILING DATE: 2005-06-20
 11 <160> NUMBER OF SEQ ID NOS: 89
 13 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
 Corrected Diskette Needed
 CPS.1-6)

ERRORED SEQUENCES

15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 36
 17 <212> TYPE: DNA
 18 <213> ORGANISM: Artificial Sequence
 W--> 19 <220> FEATURE: PLS insert mandatory <220>, whenever <221>, <222> or <223> is present.
 19 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence MoB323
 E--> 20 <400> SEQUENCE: 1
 21 tttctgcctg tcttgg
 22 36

24 <210> SEQ ID NO: 2
 25 <211> LENGTH: 26
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Artificial Sequence
 W--> 28 <220> FEATURE: SAME error
 28 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence MoB349
 E--> 29 <400> SEQUENCE: 2
 30 tttccatggg tgcagcctgg gaccac
 31 26

33 <210> SEQ ID NO: 3
 34 <211> LENGTH: 23
 35 <212> TYPE: DNA
 36 <213> ORGANISM: Artificial Sequence
 W--> 37 <220> FEATURE: SAME error
 37 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence GNT(d)1
 E--> 38 <400> SEQUENCE: 3
 39 gtttctgctg ttttctgctg ggc
 40 23

42 <210> SEQ ID NO: 4
 43 <211> LENGTH: 27
 44 <212> TYPE: DNA
 45 <213> ORGANISM: Artificial Sequence
 W--> 46 <220> FEATURE: SAME error
 PLS explain "N" locations. PLS see error explanation on page 7.

RAW SEQUENCE LISTING

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Input Set: E:\05-06-06-1041WO.txt

Output Set: N:\CRF4\06292005\J539725.raw

46 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence GTN(d)3
 E--> 47 <400> SEQUENCE: 4
 E--> 48 ~~cccttctatg cagctctg gacnco~~
 49 27
 51 <210> SEQ ID NO: 5
 52 <211> LENGTH: 25
 53 <212> TYPE: DNA
 54 <213> ORGANISM: Artificial Sequence
 W--> 55 <220> FEATURE: *Same error*
 55 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence GTN(d)2
 E--> 56 <400> SEQUENCE: 5
 E--> 57 ~~tayaaratgc agcdaytaya artgg~~
 58 25
 60 <210> SEQ ID NO: 6
 61 <211> LENGTH: 23
 62 <212> TYPE: DNA
 63 <213> ORGANISM: Artificial Sequence
 W--> 64 <220> FEATURE: *Same error*
 64 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence GTN(d)4
 E--> 65 <400> SEQUENCE: 6
 E--> 66 ~~arrtaytgyt traaraaytg ncc~~
 67 23
 69 <210> SEQ ID NO: 7
 70 <211> LENGTH: 20
 71 <212> TYPE: DNA
 72 <213> ORGANISM: Artificial Sequence
 W--> 73 <220> FEATURE: *Same error*
 73 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence 5RACEG3
 E--> 74 <400> SEQUENCE: 7
 E--> 75 ~~gtcgtgtcc aataaaggag~~
 76 20
 78 <210> SEQ ID NO: 8
 79 <211> LENGTH: 21
 80 <212> TYPE: DNA
 81 <213> ORGANISM: Artificial Sequence
 W--> 82 <220> FEATURE: *Same error*
 82 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence 5RACEG4
 E--> 83 <400> SEQUENCE: 8
 E--> 84 ~~gtcgggagag atttccatgt c~~
 85 21
 87 <210> SEQ ID NO: 9
 88 <211> LENGTH: 20
 89 <212> TYPE: DNA
 90 <213> ORGANISM: Artificial Sequence
 W--> 91 <220> FEATURE: *Same error*
 91 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence 5RACEG5
 E--> 92 <400> SEQUENCE: 9
 E--> 93 ~~ctaagatgac gacccttcgg~~
 94 20

RAW SEQUENCE LISTING

DATE: 06/29/2005

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TIME: 14:07:59

Input Set: E:\05-06-06_1041WO.txt

Output Set: N:\CRF4\06292005\J539725.raw

Same errors

96 <210> SEQ ID NO: 10
97 <211> LENGTH: 22
98 <212> TYPE: DNA
99 <213> ORGANISM: Artificial Sequence
W--> 100 <220> FEATURE:
100 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence 5RACE6
E--> 101 <400> SEQUENCE: 10
102 catcctgaga aacaaaaagt gg
103 22
105 <210> SEQ ID NO: 11
106 <211> LENGTH: 21
107 <212> TYPE: DNA
108 <213> ORGANISM: Artificial Sequence
W--> 109 <220> FEATURE:
109 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence 5RACE7
E--> 110 <400> SEQUENCE: 11
111 agttacagac ttcaatgtac g
112 21
114 <210> SEQ ID NO: 12
115 <211> LENGTH: 20
116 <212> TYPE: DNA
117 <213> ORGANISM: Artificial Sequence
W--> 118 <220> FEATURE:
118 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence 5RACE8
E--> 119 <400> SEQUENCE: 12
120 aatcaggacg gttgcaagcc
121 20
123 <210> SEQ ID NO: 13
124 <211> LENGTH: 20
125 <212> TYPE: DNA
126 <213> ORGANISM: Artificial Sequence
W--> 127 <220> FEATURE:
127 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence 3RACEG1
E--> 128 <400> SEQUENCE: 13
129 ttatccgacc tgaagtttgc
130 20
132 <210> SEQ ID NO: 14
133 <211> LENGTH: 20
134 <212> TYPE: DNA
135 <213> ORGANISM: Artificial Sequence
W--> 136 <220> FEATURE:
136 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence 3RACEG2
E--> 137 <400> SEQUENCE: 14
138 gacatacaat tttggagagc
139 20
141 <210> SEQ ID NO: 15
142 <211> LENGTH: 20
143 <212> TYPE: DNA
144 <213> ORGANISM: Artificial Sequence

RAW SEQUENCE LISTING

DATE: 06/29/2005

PATENT APPLICATION: US/10/539,725

TIME: 14:07:59

Input Set : E:\05-06-06-1041WO.txt

Output Set: N:\CRF4\06292005\J539725.raw

Same errors

W--> 145 <220> FEATURE:

E 145 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence GNT5F

E 146 <400> SEQUENCE: 15

E--> 147 cggctttaa cacaactttt

148 20

150 <210> SEQ ID NO: 16

151 <211> LENGTH: 19

152 <212> TYPE: DNA

153 <213> ORGANISM: Artificial Sequence

W--> 154 <220> FEATURE:

E 154 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence GTN6R

E 155 <400> SEQUENCE: 16

E--> 156 gccctaagct tgatccctg

157 19

159 <210> SEQ ID NO: 17

160 <211> LENGTH: 21

161 <212> TYPE: DNA

162 <213> ORGANISM: Artificial Sequence

W--> 163 <220> FEATURE:

E 163 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence GNT21F

E 164 <400> SEQUENCE: 17

E--> 165 atggcagata tggctcgatt g

166 21

168 <210> SEQ ID NO: 18

169 <211> LENGTH: 22

170 <212> TYPE: DNA

171 <213> ORGANISM: Artificial Sequence

W--> 172 <220> FEATURE:

E 172 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence GNT15R

E 173 <400> SEQUENCE: 18

E--> 174 agttttctatg gtatctaact gc

175 22

177 <210> SEQ ID NO: 19

178 <211> LENGTH: 21

179 <212> TYPE: DNA

180 <213> ORGANISM: Artificial Sequence

W--> 181 <220> FEATURE:

E 181 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence GNTHT7

E 182 <400> SEQUENCE: 19

E--> 183 gaggatccaa gtttgacctg g

184 21

186 <210> SEQ ID NO: 20

187 <211> LENGTH: 22

188 <212> TYPE: DNA

189 <213> ORGANISM: Artificial Sequence

W--> 190 <220> FEATURE:

E 190 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence GNTET7

E 191 <400> SEQUENCE: 20

E--> 192 gcaccgtgaa ttcttctag, tt

RAW SEQUENCE LISTING

DATE: 06/29/2005

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TIME: 14:07:59

Input Set: E:\05-06-06-1041WO.txt

Output Set: N:\CRF4\06292005\J539725.raw

193:22
 780 <210> SEQ ID NO: 86
 781 <211> LENGTH: 815
 782 <212> TYPE: DNA
 783 <213> ORGANISM: Artificial Sequence
 W--> 784 <220> FEATURE:
 784 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR product
 E--> 785 <400> SEQUENCE: 86

E--> 786 gttccggt gatccggtt tcatatcagt gtattatcat cagtgactgc atattgacac
 787 60
 E--> 788 caattctga tgatttttta tttttattt tttatttttt ttggtatggt tacatgcttt
 789 120
 E--> 790 ttagagggtt ctatgccgt gagtattttc ctgaatcgcg aggtgtgaca gggtatctgc
 791 180
 E--> 792 ggcgtccacc caatatttta tgatgagtcg atgattcggt agactaatct agcttaacct
 793 240
 E--> 794 ttctcttact ggcaagtcaa aattgagttt aaaatatttc agtatcctgt tagtaatttc
 795 300
 E--> 796 agaacatgt attctatgtc tcatactctt tacgtgaaag ttaactgac ttatatatttg
 797 360
 E--> 798 tggttttct gtagatcact gttttagcgc atacaaagac aattgtctaa atatttttaa
 799 420
 E--> 800 agaagtgat attttattat aagatagaag tcaatatggt tttttgttat gcacatgact
 801 480
 E--> 802 tgaataaaat aaattttttt gttagattta aatacttttt gaattatagc tttgttgaaa
 803 540
 E--> 804 ttaaggaatt tatattcata agaagctact cgaacaaatt tacaagaga acatttgata
 805 600
 E--> 806 agtaaaagta attaaaagtt ttttttaatt taaaagatt aatttttatt aataagaaga
 807 660
 E--> 808 atttgaaag ttagaaaaat atttaacttt aaaaattaag aaaacaaggc aaaactttaa
 809 720
 E--> 810 ttacaaata cttaatgtag attaattttc ttattatata ttagcacaaa ttatcattat
 811 780
 E--> 812 gtatatttt atgttattgt tacgtagagc tcaaa
 813 815

833 <210> SEQ ID NO: 89
 834 <211> LENGTH: 882
 835 <212> TYPE: DNA
 836 <213> ORGANISM: Artificial Sequence
 W--> 837 <220> FEATURE:
 837 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR product
 E--> 838 <400> SEQUENCE: 89
 E--> 839 cgggttaact ctctctatct ctctctgtgt tgcgtttgat cagggggttt aggggttggg
 840 60
 E--> 841 tccagggttc cgaggagtat cgtcacgtgt attgcggtct tgttgagat tctcagttg
 842 120
 E--> 843 tgcattgaga tataaactta gtttagtcca cgatcggttt ctaatcgtgg atttttgtgg
 844 180

See item # 11 on error
 summary sheet

See
 item
 # 1 on
 error
 summary
 sheet.

Same error

RAW SEQUENCE LISTING

DATE: 06/29/2005

PATENT APPLICATION: US/10/539,725

TIME: 14:08:00

Input Set: E:\05-06-06\1041WO.txt

Output Set: N:\CRF4\06292005\J539725.raw

E--> 845 atttcgggtcg ttgagcaaga atttttgtgaa ttttttgtat tgggggaagg aaatggggtt
846 240
E--> 847 atggcgatat cgttttgggtt ggggttcaacg tgatcgggtga gctocaggaa gggctggtca
848 300
E--> 849 ctcaacaatcc ggtattcgtc tcatcgagac gcatttatcg gttcattata tgtatatata
850 360
E--> 851 tatatatata tatatgcaga gtogattgtg ttgcaatttc tgaactaggt actgttgaat
852 420
E--> 853 tctagattgc cttcaagtag ctctcgatgt tggaaatgacg sacacaaatt ctgctactga
854 480
E--> 855 atgagaccat attctgcacc gtttaattggt tttatgaata tatggtgtcg aattacattc
856 540
E--> 857 agctcgaat ccatgcgcc tttctgcacg aacgttggtt tgtagttgta gtgcagccag
858 600
E--> 859 tctgtttggt ttaggattat gctttgacga tcgatgagtc cgtttcatgg ttttataact
860 660
E--> 861 gtaatttata ttcttgtgat tttttgttta caaatgttcc cccaattgta acgtgggact
862 720
E--> 863 tctgtgtgtg gtggttgctc aaattgatag ttttggtcat ttgatttgcg gagagcaatc
864 780
E--> 865 ggtgtcatgg aaaatccctt cgaactgctt gatccaatca aagttctgct tgagccaatg
866 840
E--> 867 tggaggtgg aggattgggc ttcttctaag tgagaattct cg
868 882

↑
SAME ERRORS

↑
The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

VARIABLE LOCATION SUMMARY

DATE: 06/29/2005

PATENT APPLICATION: US/10/539,725

TIME: 14:08:01

Input Set: E:\05-06-06 1041WO.txt

Output Set: N:\CRF4\06292005\J539725.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:3; N Pos. 3,6,9,12,15,18

Seq#:4; N Pos. 9,12,15,19,22,25

Seq#:5; N Pos. 9,13

Seq#:6; N Pos. 21

Seq#:31; N Pos. 6

Seq#:32; N Pos. 3,6,9,12,15

Seq#:33; N Pos. 3,6,9

Seq#:55; N Pos. 9,18

Seq#:56; N Pos. 3,6,15

Seq#:57; N Pos. 3,6,15,21

VERIFICATION SUMMARY

DATE: 06/29/2005

PATENT APPLICATION: US/10/539,725

TIME: 14:08:01

Input-Set : E:\05-06-06-1041WO.txt

Output-Set: N:\CRF4\06292005\J539725.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:19 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:20 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:1
L:20 M:283 W: Missing Blank Line separator, <400> field identifier
L:21 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:36 SEQ:1
L:28 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:29 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:2
L:29 M:283 W: Missing Blank Line separator, <400> field identifier
L:30 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:2
L:37 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:38 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:3
L:38 M:283 W: Missing Blank Line separator, <400> field identifier
L:39 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:3
L:39 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:3
L:39 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:39 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:3
L:46 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:47 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:4
L:47 M:283 W: Missing Blank Line separator, <400> field identifier
L:48 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:4
L:48 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:4
L:48 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:48 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:27 SEQ:4
L:55 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:56 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:5
L:56 M:283 W: Missing Blank Line separator, <400> field identifier
L:57 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:5
L:57 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5
L:57 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:57 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:5
L:64 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:65 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:6
L:65 M:283 W: Missing Blank Line separator, <400> field identifier
L:66 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:6
L:66 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:6
L:66 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:66 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:6
L:73 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:74 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:7
L:74 M:283 W: Missing Blank Line separator, <400> field identifier
L:75 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:7
L:82 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:83 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:8
L:83 M:283 W: Missing Blank Line separator, <400> field identifier
L:84 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:8
L:91 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:92 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:9

VERIFICATION SUMMARY

DATE: 06/29/2005

PATENT APPLICATION: US/10/539,725

TIME: 14:08:01

Input Set: E:\05-06-06-11041WO.txt

Output Set: N\CRF4\06292005\J539725.raw

L:92 M:283 W: Missing Blank Line separator, <400> field identifier
L:93 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:9
L:100 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:101 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:10
L:101 M:283 W: Missing Blank Line separator, <400> field identifier
L:102 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:10
L:109 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:110 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:11
L:110 M:283 W: Missing Blank Line separator, <400> field identifier
L:111 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:11
L:118 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:119 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:12
L:119 M:283 W: Missing Blank Line separator, <400> field identifier
L:120 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:12
L:127 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:128 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:13
L:128 M:283 W: Missing Blank Line separator, <400> field identifier
L:129 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:13
L:136 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:137 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:14
L:137 M:283 W: Missing Blank Line separator, <400> field identifier
L:138 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:14
L:145 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:15
L:146 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:15
L:146 M:283 W: Missing Blank Line separator, <400> field identifier
L:147 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:15
L:154 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
L:155 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:16
L:155 M:283 W: Missing Blank Line separator, <400> field identifier
L:156 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:16
L:163 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:164 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:17
L:164 M:283 W: Missing Blank Line separator, <400> field identifier
L:165 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:17
L:172 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
L:173 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:18
L:173 M:283 W: Missing Blank Line separator, <400> field identifier
L:174 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:18
L:181 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:182 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:19
L:182 M:283 W: Missing Blank Line separator, <400> field identifier
L:183 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:19
L:190 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:191 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:20
L:191 M:283 W: Missing Blank Line separator, <400> field identifier
L:192 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:20
L:199 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21
L:200 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:21
L:200 M:283 W: Missing Blank Line separator, <400> field identifier

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Input Set : E:\05-06-06-1041WO.txt

Output Set: N:\CRF4\06292005\J539725.raw

L:201 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:21
L:208 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22
L:209 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:22
L:209 M:283 W: Missing Blank Line separator, <400> field identifier
L:210 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:22
L:217 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23
L:218 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:23
L:218 M:283 W: Missing Blank Line separator, <400> field identifier
L:219 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:23
L:226 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
L:227 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:24
L:227 M:283 W: Missing Blank Line separator, <400> field identifier
L:228 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:24
L:235 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:25
L:236 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:25
L:236 M:283 W: Missing Blank Line separator, <400> field identifier
L:237 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:25
L:244 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:245 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:26
L:245 M:283 W: Missing Blank Line separator, <400> field identifier
L:246 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:26
L:253 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:27
L:254 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:27
L:254 M:283 W: Missing Blank Line separator, <400> field identifier
L:255 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:27
L:262 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:263 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:28
L:263 M:283 W: Missing Blank Line separator, <400> field identifier
L:264 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:28
L:271 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:29
L:272 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:29
L:272 M:283 W: Missing Blank Line separator, <400> field identifier
L:273 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:29
L:280 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
L:281 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:30
L:281 M:283 W: Missing Blank Line separator, <400> field identifier
L:282 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:30
L:289 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:31/
L:290 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:31
L:290 M:283 W: Missing Blank Line separator, <400> field identifier
L:291 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:31
L:291 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:31
L:291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
L:291 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:31
L:298 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32
L:299 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:32
L:299 M:283 W: Missing Blank Line separator, <400> field identifier
L:300 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:32
L:300 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:32

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L:300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0
L:300 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:32
L:307 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:33
L:308 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:33
L:308 M:283 W: Missing Blank Line separator, <400> field identifier
L:309 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:33
L:309 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:33
L:309 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
L:309 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:17 SEQ:33
L:316 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:34
L:317 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:34
L:317 M:283 W: Missing Blank Line separator, <400> field identifier
L:318 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:34
L:325 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:35
L:326 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:35
L:326 M:283 W: Missing Blank Line separator, <400> field identifier
L:327 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:35
L:334 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36
L:335 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:36
L:335 M:283 W: Missing Blank Line separator, <400> field identifier
L:336 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:36
L:344 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:37
L:344 M:283 W: Missing Blank Line separator, <400> field identifier
L:345 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:37
L:353 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:38
L:353 M:283 W: Missing Blank Line separator, <400> field identifier
L:354 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:38
L:362 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:39
L:362 M:283 W: Missing Blank Line separator, <400> field identifier
L:363 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:39
L:371 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:40
L:371 M:283 W: Missing Blank Line separator, <400> field identifier
L:372 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:40
L:380 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:41
L:380 M:283 W: Missing Blank Line separator, <400> field identifier
L:381 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:41
L:389 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:42
L:389 M:283 W: Missing Blank Line separator, <400> field identifier
L:390 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:42
L:398 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:43
L:398 M:283 W: Missing Blank Line separator, <400> field identifier
L:399 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:43
L:407 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:44
L:407 M:283 W: Missing Blank Line separator, <400> field identifier
L:408 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:44
L:416 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:45
L:416 M:283 W: Missing Blank Line separator, <400> field identifier
L:417 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:45
L:425 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:46

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L:425 M:283 W: Missing Blank Line separator, <400> field identifier
L:426 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:46
L:434 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:47
L:434 M:283 W: Missing Blank Line separator, <400> field identifier
L:435 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:47
L:443 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:48
L:443 M:283 W: Missing Blank Line separator, <400> field identifier
L:444 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:48
L:452 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:49
L:452 M:283 W: Missing Blank Line separator, <400> field identifier
L:453 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:49
L:461 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:50
L:461 M:283 W: Missing Blank Line separator, <400> field identifier
L:462 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:50
L:507 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55 after pos.:0
L:516 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:0
L:525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:0